

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/030,606DATE: 03/07/98
TIME: 15:45:50

INPUT SET: S2902.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

SEQUENCE LISTING

ENTERED

(1) General Information:

(i) APPLICANTS: Xu, Jiangchun
Dillon, Davin C.

(ii) TITLE OF INVENTION: COMPOUNDS FOR IMMUNODIAGNOSIS OF PROSTATE CANCER AND METHO

(iii) NUMBER OF SEQUENCES: 224

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: SEED and BERRY LLP
(B) STREET: 6300 Columbia Center, 701 Fifth Avenue
(C) CITY: Seattle
(D) STATE: WA
(E) COUNTRY: USA
(F) ZIP: 98104

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE: 25-FEB-1998
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Maki, David J.
(B) REGISTRATION NUMBER: 31,392
(C) REFERENCE/DOCKET NUMBER: 210121.428C3

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (206) 622-4900
(B) TELEFAX: (206) 682-6031

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 814 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/030,606DATE: 03/07/98
TIME: 15:45:52

INPUT SET: S2902.raw

47 (D) TOPOLOGY: linear

48

49 (ii) MOLECULE TYPE: cDNA

50

51 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

52

| | | | | | | | |
|----|-------------|------------|------------|------------|------------|-------------|-----|
| 53 | TTTTTTTTTTT | TTTTTCACAG | TATAACAGCT | CTTTATTTCT | GTGAGTTCTA | CTAGGAAATC | 60 |
| 54 | ATCAAATCTG | AGGGTTGTCT | GGAGGACTTC | AATACACCTC | CCCCCATAGT | GAATCAGCTT | 120 |
| 55 | CCAGGGGGTC | CAGTCCCTCT | CCTTACTTCA | TCCCCATCCC | ATGCCAAAGG | AAGACCCTCC | 180 |
| 56 | CTCCTTGGCT | CACAGCCTTC | TCTAGGCTTC | CCAGTGCCTC | CAGGACAGAG | TGGGTTATGT | 240 |
| 57 | TTTCAGCTCC | ATCCTTGCTG | TGAGTGTCTG | GTGCGTTGTG | CCTCCAGCTT | CTGCTCAGTG | 300 |
| 58 | CTTCATGGAC | AGTGTCAGC | ACATGTCACT | CTCCACTCTC | TCAGTGTGGA | TCCACTAGTT | 360 |
| 59 | CTAGAGCGGC | CGCCACCGCG | GTGGAGCTCC | AGCTTTTGTT | CCCTTTAGTG | AGGGTTAATT | 420 |
| 60 | GCGCGCTTGG | CGTAATCATG | GTCATAACTG | TTTCCTGTGT | GAAATTGTTA | TCCGCTCACA | 480 |
| 61 | ATTCCACACA | ACATACGAGC | CGGAAGCATA | AAGTGTAAG | CCTGGGGTGC | CTAATGAGTG | 540 |
| 62 | ANCTAACTCA | CATTAATTGC | GTTGCGCTCA | CTGNCCGCTT | TCCAGTCNGG | AAAAGTGTCTG | 600 |
| 63 | TGCCAGCTGC | ATTAATGAAT | CGGCCAACGC | NCGGGGAAAA | GCGGTTTGCG | TTTTGGGGGC | 660 |
| 64 | TCTTCCGCTT | CTCGCTCACT | NANTCCTGCG | CTCGGTCNTT | CGGCTGCGGG | GAACGGTATC | 720 |
| 65 | ACTCCTCAAA | GGNGGTATTA | CGGTTATCCN | NAAATCNGGG | GATACCCNGG | AAAAAANTTT | 780 |
| 66 | AACAAAAGGG | CANCAAAGGG | CNGAAACGTA | AAAA | | | 814 |

67

68 (2) INFORMATION FOR SEQ ID NO:2:

69

70 (i) SEQUENCE CHARACTERISTICS:

71 (A) LENGTH: 816 base pairs

72 (B) TYPE: nucleic acid

73 (C) STRANDEDNESS: single

74 (D) TOPOLOGY: linear

75

76 (ii) MOLECULE TYPE: cDNA

77

78 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

79

| | | | | | | | |
|----|------------|------------|-------------|------------|-------------|------------|-----|
| 80 | ACAGAAATGT | TGGATGGTGG | AGCACCTTTC | TATACGACTT | ACAGGACAGC | AGATGGGGAA | 60 |
| 81 | TTCATGGCTG | TTGGAGCAAT | AGAACCCCAG | TTCTACGAGC | TGCTGATCAA | AGGACTTGGA | 120 |
| 82 | CTAAAGTCTG | ATGAACTTCC | CAATCAGATG | AGCATGGATG | ATTGGCCAGA | AATGAAGAAG | 180 |
| 83 | AAGTTTGCAG | ATGTATTTGC | AAAGAAGACG | AAGGCAGAGT | GGTGTCAAAT | CTTTGACGGC | 240 |
| 84 | ACAGATGCCT | GTGTGACTCC | GGTTCTGACT | TTTGAGGAGG | TTGTTTCATCA | TGATCACAAC | 300 |
| 85 | AAGGAACGGG | GCTCGTTTAT | CACCAGTGAG | GAGCAGGACG | TGAGCCCCCG | CCCTGCACCT | 360 |
| 86 | CTGCTGTAA | ACACCCCAGC | CATCCCTTCT | TTCAAAAGGG | ATCCACTAGT | TCTAGAAGCG | 420 |
| 87 | GCCGCCACCG | CGGTGGAGCT | CCAGCTTTTG | TTCCCTTTAG | TGAGGGTTAA | TTGCGCGCTT | 480 |
| 88 | GGCGTAATCA | TGGTCATAGC | TGTTTCCTGT | GTGAAATTGT | TATCCGCTCA | CAATTCCCCC | 540 |
| 89 | AACATACGAG | CCGGAACATA | AAGTGTTAAG | CCTGGGGTGC | CTAATGANTG | AGCTAACTCN | 600 |
| 90 | CATTAATTGC | GTTGCGCTCA | CTGCCCCGCTT | TCCAGTCGGG | AAAAGTGTCTG | TGCCACTGCN | 660 |
| 91 | TTANTGAATC | NGCCACCCCC | CGGGAAAAGG | CGGTTGCNTT | TTGGGCCTCT | TCCGCTTTCC | 720 |
| 92 | TCGCTCATTG | ATCCTNGCNC | CCGGTCTTCG | GCTGCGGNGA | ACGGTTCACT | CCTCAAAGGC | 780 |
| 93 | GGTNTNCCGG | TTATCCCCAA | ACNNGGGGATA | CCCNGA | | | 816 |

94

95 (2) INFORMATION FOR SEQ ID NO:3:

96

97 (i) SEQUENCE CHARACTERISTICS:

98 (A) LENGTH: 773 base pairs

99 (B) TYPE: nucleic acid

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/030,606DATE: 03/07/98
TIME: 15:45:54

INPUT SET: S2902.raw

100 (C) STRANDEDNESS: single
101 (D) TOPOLOGY: linear
102
103 (ii) MOLECULE TYPE: cDNA
104
105 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
106
107 CTTTTGAAAG AAGGGATGGC TGGGGTGTTC AACAGCAGAG GTGCAGGGCG GGGGCTCACG 60
108 TCCTGCTCCT CACTGGTGAT AAACGAGCCC CGTTCCTTGT TGTGATCATG ATGAACAACC 120
109 TCCTCAAAG TCAGAACCGG AGTCACACAG GCATCTGTGC CGTCAAAGAT TTGACACCAC 180
110 TCTGCCTTCG TCTTCTTTGC AAATACATCT GCAAACCTCT TCTTCATTTT TGGCCAATCA 240
111 TCCATGCTCA TCTGATTGGG AAGTTCATCA GACTTTAGTC CANNTCCTTT GATCAGCAGC 300
112 TCGTAGAACT GGGGTTCTAT TGCTCCAACA GCCATGAATT CCCCATCTGC TGTCTGTAA 360
113 GTCGTATAGA AAGGTGCTCC ACCATCCAAC ATGTTCTGTC CTCGAGGGGG GGCCCGGTAC 420
114 CCAATTCGCC CTATANTGAG TCGTATTACG CGCGCTCACT GGCCGTCGTT TTACAACGTC 480
115 GTGACTGGGA AAACCCTGGG CGTTACCAAC TTAATCGCCT TGCAGCACAT CCCCCTTTCG 540
116 CCAGCTGGGC GTAATANCGA AAAGGCCCGC ACCGATCGCC CTTCCAACAG TTGCGCACCT 600
117 GAATGGGNAA ATGGGACCCC CCTGTTACCG CGCATTNAAC CCCC GCNNGG TTTNGTTGTT 660
118 ACCCCACANT NNACCCTTA CACTTTGCCA GCGCCTTANC GCCCGCTCCC TTTNCCTTT 720
119 CTTCCCTTCC TTTNCNCCN CTTTCCCCCG GGGTTTCCCC CNTCAAACCC CNA 773
120
121 (2) INFORMATION FOR SEQ ID NO:4:
122
123 (i) SEQUENCE CHARACTERISTICS:
124 (A) LENGTH: 828 base pairs
125 (B) TYPE: nucleic acid
126 (C) STRANDEDNESS: single
127 (D) TOPOLOGY: linear
128
129 (ii) MOLECULE TYPE: cDNA
130
131 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:
132
133 CCTCCTGAGT CCTACTGACC TGTGCTTTCT GGTGTGGAGT CCAGGGCTGC TAGGAAAAGG 60
134 AATGGGCAGA CACAGGTGTA TGCCAATGTT TCTGAAATGG GTATAATTTT GTCCTCTCCT 120
135 TCGGAACACT GGCTGTCTCT GAAGACTTCT CGCTCAGTTT CAGTGAGGAC ACACACAAAG 180
136 ACGTGGGTGA CCATGTTGTT TGTGGGGTGC AGAGATGGGA GGGGTGGGGC CCACCCTGGA 240
137 AGAGTGGACA GTGACACAAG GTGGACACTC TCTACAGATC ACTGAGGATA AGCTGGAGCC 300
138 ACAATGCATG AGGCACACAC ACAGCAAGGA TGACNCTGTA AACATAGCCC ACGCTGTCCT 360
139 GNGGGCACTG GGAAGCCTAN ATNAGGCCGT GAGCANAAAG AAGGGGAGGA TCCACTAGTT 420
140 CTANAGCGCG CGCCACCGCG GTGGANCTCC ANCTTTTGTG CCCTTTAGTG AGGGTTAATT 480
141 GCGCGCTTGG CNTAATCATG GTCATANCTN TTTCTGTGT GAAATTGTTA TCCGCTCACA 540
142 ATTCCACACA ACATACGANC CGGAAACATA AANTGTAAAC CTGGGGTGCC TAATGANTGA 600
143 CTAATCACA TTAATTGCGT TGCCTCACT GCCCGCTTTC CAATCNGGAA ACCTGTCTTG 660
144 CCNCTTGAT TNATGAATCN GCCAACCCCC GGGGAAAAGC GTTTGCGTTT TGGGCGCTCT 720
145 TCCGCTTCCT CNCTCANTTA NTCCCTNCNC TCGGTCATTC CGGCTGCNGC AAACCGGTTT 780
146 ACCNCCTCCA AAGGGGGTAT TCCGTTTCC CCNAATCCGG GGANANCC 828
147
148 (2) INFORMATION FOR SEQ ID NO:5:
149
150 (i) SEQUENCE CHARACTERISTICS:
151 (A) LENGTH: 834 base pairs
152 (B) TYPE: nucleic acid

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/030,606DATE: 03/07/98
TIME: 15:45:56

INPUT SET: S2902.raw

153 (C) STRANDEDNESS: single
154 (D) TOPOLOGY: linear
155
156 (ii) MOLECULE TYPE: cDNA
157
158 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:
159
160 TTTTTTTTTT TTTTACTGA TAGATGGAAT TTATTAAGCT TTTCACATGT GATAGCACAT 60
161 AGTTTTAATT GCATCCAAAG TACTAACAAA AACTCTAGCA ATCAAGAATG GCAGCATGTT 120
162 ATTTTATAAC AATCAACACC TGTGGCTTTT AAAATTTGGT TTTCATAAGA TAATTTATAC 180
163 TGAAGTAAAT CTAGCCATGC TTTTAAAAAA TGCTTTAGGT CACTCCAAGC TTGGCAGTTA 240
164 ACATTTGGCA TAAACAATAA TAAAACAATC ACAATTTAAT AAATAACAAA TACAACATTG 300
165 TAGGCCATAA TCATATACAG TATAAGGAAA AGGTGGTAGT GTTGAGTAAG CAGTTATTAG 360
166 AATAGAATAC CTTGGCCTCT ATGCAAATAT GTCTAGACAC TTTGATTAC TCAGCCCTGA 420
167 CATTCAAGTTT TCAAAGTAGG AGACAGGTTT TACAGTATCA TTTTACAGTT TCCAACACAT 480
168 TGA AAAACAAG TAGAAAATGA TGAGTTGATT TTTATTAATG CATTACATCC TCAAGAGTTA 540
169 TCACCAACCC CTCAGTTATA AAAAATTTTC AAGTTATATT AGTCATATAA CTTGGTGTGC 600
170 TTATTTTAAA TTAGTGCTAA ATGGATTAAG TGAAGACAAC AATGGTCCCC TAATGTGATT 660
171 GATATTGGTC ATTTTACCA GCTTCTAAAT CTNAACTTTC AGGCTTTTGA ACTGGAACAT 720
172 TGNATNACAG TGTTCCANAG TTNCAACCTA CTGGAACATT ACAGTGTGCT TGATTCAAAA 780
173 TGTTATTTTG TTA AAAAATTA AATTTTAACC TGGTGGAAAA ATAATTTGAA ATNA 834
174
175 (2) INFORMATION FOR SEQ ID NO:6:
176
177 (i) SEQUENCE CHARACTERISTICS:
178 (A) LENGTH: 818 base pairs
179 (B) TYPE: nucleic acid
180 (C) STRANDEDNESS: single
181 (D) TOPOLOGY: linear
182
183 (ii) MOLECULE TYPE: cDNA
184
185 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:
186
187 TTTTTTTTTT TTTTTTTTTT AAGACCCTCA TCAATAGATG GAGACATACA GAAATAGTCA 60
188 AACCACATCT ACAAATGCC AGTATCAGGC GCGGCTTCG AAGCCAAAGT GATGTTTGGA 120
189 TGTAAGTGA AATATTAGTT GCGGATGAA GCAGATAGTG AGGAAAGTTG AGCCAATAAT 180
190 GACGTGAAGT CCGTGGAAGC CTGTGGCTAC AAAAAATGTT GAGCCGTAGA TGCCGTCGGA 240
191 AATGGTGAAG GGAGACTCGA AGTACTCTGA GGCTTG TAGG AGGGTAAAAT AGAGACCCAG 300
192 TAAAATTGTA ATAAGCAGTG CTTGAATTAT TTGGTTTCGG TTGTTTTCTA TTAGACTATG 360
193 GTGAGCTCAG GTGATTGATA CTCCTGATGC GAGTAATACG GATGTGTTTA GGAGTGGGAC 420
194 TTCTAGGGGA TTTAGCGGGG TGATGCCTGT TGGGGGCCAG TGCCCTCCTA GTTGGGGGGT 480
195 AGGGGCTAGG CTGGAGTGGT AAAAGGCTCA GAAAAATCCT GCGAAGAAAA AAACCTCTGA 540
196 GGTAATAAAT AGGATTATCC CGTATCGAAG GCCTTTTGG ACAGGTGGTG TGTGGTGGCC 600
197 TTGGTATGTG CTTTCTCGTG TTACATCGCG CCATCATTGG TATATGGTTA GTGTGTTGGG 660
198 TTANTANGGC CTANTATGAA GAACTTTTGG ANTGGAATTA AATCAATNGC TTGGCCGGAA 720
199 GTCATTANGA NGGCTNAAAA GGCCCTGTTA NGGGTCTGGG CTNGGTTTTA CCCNACCCAT 780
200 GGAATNCNCC CCCC GGACNA NTGNATCCCT ATTCTTAA 818
201
202 (2) INFORMATION FOR SEQ ID NO:7:
203
204 (i) SEQUENCE CHARACTERISTICS:
205 (A) LENGTH: 817 base pairs

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/030,606DATE: 03/07/98
TIME: 15:45:58

INPUT SET: S2902.raw

206 (B) TYPE: nucleic acid
207 (C) STRANDEDNESS: single
208 (D) TOPOLOGY: linear
209

210 (ii) MOLECULE TYPE: cDNA
211

212 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:
213

| | | | | | | | |
|-----|------------|------------|------------|------------|-------------|------------|-----|
| 214 | TTTTTTTTTT | TTTTTTTTTT | TGGCTCTAGA | GGGGGTAGAG | GGGGTGCTAT | AGGGTAAATA | 60 |
| 215 | CGGGCCCTAT | TTCAAAGATT | TTTAGGGGAA | TTAATTCTAG | GACGATGGGT | ATGAAACTGT | 120 |
| 216 | GGTTTGCTCC | ACAGATTTCA | GAGCATTGAC | CGTAGTATAC | CCCCGGTCGT | GTAGCGGTGA | 180 |
| 217 | AAGTGGTTTG | GTTTAGACGT | CCGGGAATTG | CATCTGTTTT | TAAGCCTAAT | GTGGGGACAG | 240 |
| 218 | CTCATGAGTG | CAAGACGTCT | TGTGATGTAA | TTATTATACN | AATGGGGGCT | TCAATCGGGA | 300 |
| 219 | GTACTACTCG | ATTGTCAACG | TCAAGGAGTC | GCAGGTCGCC | TGGTTCCTAGG | AATAATGGGG | 360 |
| 220 | GAAGTATGTA | GGAATTGAAG | ATTAATCCGC | CGTAGTCGGT | GTTCTCCTAG | GTTCAATACC | 420 |
| 221 | ATTGGTGGCC | AATTGATTTG | ATGGTAAGGG | GAGGGATCGT | TGAACTCGTC | TGTTATGTAA | 480 |
| 222 | AGGATNCCTT | NGGGATGGGA | AGGCNATNAA | GGACTANGGA | TNAATGGCGG | GCANGATATT | 540 |
| 223 | TCAAACNGTC | TCTANTTCCT | GAAACGTCTG | AAATGTTAAT | AANAATTAAN | TTTNGTTATT | 600 |
| 224 | GAATNTTNG | GAAAAGGGCT | TACAGGACTA | GAAACCAAT | ANGAAAANTA | ATNNTAANGG | 660 |
| 225 | CNTTATCNTN | AAAGGTNATA | ACCNCTCCTA | TNATCCCACC | CAATNGNATT | CCCCACNCNN | 720 |
| 226 | ACNATTGGAT | NCCCCANTTC | CANAAANGGC | CNCCCCCGG | TGNANNCCNC | CTTTTGTTCC | 780 |
| 227 | CTTNANTGAN | GGTTATTCNC | CCCTNGCNTT | ATCANCC | | | 817 |

228
229 (2) INFORMATION FOR SEQ ID NO:8:
230

231 (i) SEQUENCE CHARACTERISTICS:
232 (A) LENGTH: 799 base pairs
233 (B) TYPE: nucleic acid
234 (C) STRANDEDNESS: single
235 (D) TOPOLOGY: linear
236

237 (ii) MOLECULE TYPE: cDNA
238

239 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:
240

| | | | | | | | |
|-----|------------|------------|------------|------------|------------|------------|-----|
| 241 | CATTTCGGG | TTTACTTTCT | AAGGAAAGCC | GAGCGGAAGC | TGCTAACGTG | GGAATCGGTG | 60 |
| 242 | CATAAGGAGA | ACTTTCTGCT | GGCACGCGCT | AGGGACAAGC | GGGAGAGCGA | CTCCGAGCGT | 120 |
| 243 | CTGAAGCGCA | CGTCCCAGAA | GGTGGACTTG | GCACTGAAAC | AGCTGGGACA | CATCCGCGAG | 180 |
| 244 | TACGAACAGC | GCCTGAAAGT | GCTGGAGCGG | GAGGTCCAGC | AGTGTAGCCG | CGTCCTGGGG | 240 |
| 245 | TGGGTGGCCG | ANGCCTGANC | CGCTCTGCCT | TGCTGCCCCC | ANGTGGGCCG | CCACCCCTTG | 300 |
| 246 | ACCTGCCTGG | GTCCAAACAC | TGAGCCCTGC | TGGCGGACTT | CAAGGANAAC | CCCCACANGG | 360 |
| 247 | GGATTTTGCT | CCTANANTAA | GGCTCATCTG | GGCCTCGGCC | CCCCCACCTG | GTTGGCCTTG | 420 |
| 248 | TCTTTGANGT | GAGCCCCATG | TCCATCTGGG | CCACTGTCNG | GACCACCTTT | NGGGAGTGTT | 480 |
| 249 | CTCCTTACAA | CCACANNATG | CCCGGCTCCT | CCCGGAAACC | ANTCCCANCC | TGNGAAGGAT | 540 |
| 250 | CAAGNCCTGN | ATCCACTNNT | NCTANAACCG | GCCNCCNCCG | CNGTGGAACC | CNCCTTNTGT | 600 |
| 251 | TCCTTTTCNT | TNAGGGTTAA | TMNCGCCTTG | GCCTTNCCAN | NGTCCTNCNC | NTTTTCCNNT | 660 |
| 252 | GTTNAAATTG | TTANGCNCCC | NCCNNTCCCN | CNCCNCCNAN | CCCGACCCNN | ANNTTNNANN | 720 |
| 253 | NCCTGGGGGT | NCCNNCNGAT | TGACCCNCC | NCCCTNTANT | TGCNTTNGGG | NNCNNTGCCC | 780 |
| 254 | CTTTCCTCT | NGGGANNCG | | | | | 799 |

255
256 (2) INFORMATION FOR SEQ ID NO:9:
257

258 (i) SEQUENCE CHARACTERISTICS:

PAGE: 1

SEQUENCE VERIFICATION REPORT
PATENT APPLICATION *US/09/030,606*

DATE: 03/07/98
TIME: 15:46:00

INPUT SET: S2902.raw

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Original Text